(b) adding a nuclease to the sample to digest free target nucleic acids in the sample to form a digested sample;

(c) determining a total target nucleic acid content remaining in the digested sample; and

(d) quantifying the total amount of free target nucleic acid in the sample by subtracting the determined amount of target nucleic acid content in the digested sample from the determined amount of total target nucleic acid content in the sample.

2. (Amended) The method of claim 1, wherein the determining of the target nucleic acids is performed using a nucleic acid amplification assay.

3. (Amended) The method of claim 2, wherein the nucleic acid amplification assay is a polymerase chain reaction (PCR) assay or a reverse transcriptase (RT) PCR assay.

4. (Amended) The method of claim 1, further comprising adding a nucleic acid standard to the sample before the total target nucleic acid content of (a) is determined.

5. (Amended) The method of claim 1, further comprising adding a nucleic acid standard to the sample after the free target nucleic acids in the sample are digested with the nuclease.

6. (Amended) The method of claim 1, wherein the nuclease is inactivated after the free nucleic acids in the sample are digested.

7. (Amended) The method of claim 1, wherein the nuclease is a DNase or an RNase.

C1 cont'd

8. (Amended) The method of claim 1, wherein the sample is selected from the group consisting of blood, plasma, serum, cell culture fluids, cells and a pharmaceutical preparation.

C2

21. (New) A method for determining the proportions of infectious pathogens and inactivated pathogens in a sample, wherein the method is capable of differentiating free and encapsulated target nucleic acids in the sample, wherein the method comprises

(a) determining a total target nucleic acid content in the sample;

(b) adding a nuclease to the sample to digest free target nucleic acids in the sample to form a digested sample, wherein the nuclease will not digest the encapsulated target nucleic acids;

(c) determining a total target nucleic acid content remaining in the digested sample, which represents the amount of infectious pathogens in the sample;

(d) quantifying the total amount of free target nucleic acid in the sample by subtracting the determined amount of target nucleic acid content in the digested sample

from the determined amount of total target nucleic acid content in the sample, wherein the quantifying indicates the amount of inactivated pathogens in the sample.

22. (New) The method of claim 21, wherein the determining of the target nucleic acids is performed using a nucleic acid amplification assay.

Q2

23. (New) The method of claim 22, wherein the nucleic acid amplification assay is a polymerase chain reaction (PCR) assay or a reverse transcriptase (RT) PCR assay.

24. (New) The method of claim 21, further comprising adding a nucleic acid standard to the sample before the total target nucleic acid content of (a) is determined.

25. (New) The method of claim 21, further comprising adding a nucleic acid standard to the sample after the free target nucleic acids in the sample are digested with the nuclease.

26. (New) The method of claim 21, wherein the nuclease is inactivated after the free nucleic acids in the sample are digested.

27. (New) The method of claim 21, wherein the nuclease is a DNase or an RNase.

28. (New) The method of claim 21, wherein the sample is selected from the group consisting of blood, plasma, serum, cell culture fluids, cells and a pharmaceutical preparation.

29. (New) The method according to claim 21, wherein the pathogen is a virus.

Cl2

30. (New) The method according to claim 29, wherein the virus is selected from the group consisting of parvovirus, hepatitis virus and human immunodeficiency virus.

31. (New) A method for detecting infectious pathogens in a sample, wherein the method comprises

(a) determining a total target nucleic acid content in the sample;

(b) adding a nuclease to the sample to digest any free target nucleic acids in the sample to form a digested sample, wherein the nuclease will not digest the encapsulated target nucleic acids; and

(c) determining a total target nucleic acid content remaining in the digested sample, which represents the amount of infectious pathogens in the sample.

32. (New) The method of claim 31, wherein the determining of the target nucleic acids is performed using a nucleic acid amplification assay.

33. (New) The method of claim 32, wherein the nucleic acid amplification assay is a polymerase chain reaction (PCR) assay or a reverse transcriptase (RT) PCR assay.

34. (New) The method of claim 31, further comprising adding a nucleic acid standard to the sample before the total target nucleic acid content of (a) is determined.

a2

35. (New) The method of claim 31, further comprising adding a nucleic acid standard to the sample after the free target nucleic acids in the sample are digested with the nuclease.

36. (New) The method of claim 31, wherein the nuclease is inactivated after the free nucleic acids in the sample are digested.

37. (New) The method of claim 31, wherein the nuclease is a DNase or an RNase.

39. (New) The method of claim 31, wherein the sample is selected from the group consisting of blood, plasma, serum, cell culture fluids, cells and a pharmaceutical preparation.

40. (New) The method according to claim 31, wherein the pathogen is a virus.

A2 cont.)

41. (New) The method according to claim 40, wherein the virus is selected from the group consisting of parvovirus, hepatitis virus and human immunodeficiency virus.